

SEQUENCE LISTING



<110> Lukyanov, Sergey  
Lukyanov, Konstantin  
Yanushevich, Yuriy  
Savistky, Alexandr  
Fradkov, Arcady

<120> Non Aggregating Fluorescent Proteins and  
Methods for Using the Same

<130> CLON-067

<150> 10/006,922

<151> 2001-12-04

<150> 60/270,983

<151> 2001-02-21

<160> 31

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 687

<212> DNA

<213> Anemonia majano

<400> 1

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acgcagacct cgacttttaa agtcaccatg gccaacggtg ggccccttgc attctccttt 180
gacatactat ctacagtgtt caagtatgga aatcgatgct ttactgcgta tcctaccagt 240
atgcccgaact atttcaaaca agcatttcct gacggaatgt catatgaaag gacttttacc 300
tatgaagatg gaggagtgtc tacagccagt tgggaaataa gccttaaagg caactgcttt 360
gagcaciaat ccacgtttca tggagtgaac tttcctgctg atggacctgt gatggcgaag 420
atgacaactg gttgggaccc atcttttgag aaaatgactg tctgcatggt aatattgaag 480
ggtgatgtca ccgcgttcct catgctgcaa ggaggtggca attacagatg ccaattccac 540
acttcttaca agacaaaaaa accggtgacg atgccaccaa accatgcggt ggaacatcgc 600
attgcgagga ccgaccttga caaaggtggc aacagtgttc agctgacgga gcacgctgtt 660
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<210> 2

<211> 229

<212> PRT

<213> Anemonia majano

<400> 2

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          20             25             30
Gly Asn Gly Lys Pro Tyr Glu Gly Thr Gln Thr Ser Thr Phe Lys Val
          35             40             45
Thr Met Ala Asn Gly Gly Pro Leu Ala Phe Ser Phe Asp Ile Leu Ser
          50             55             60
Thr Val Phe Lys Tyr Gly Asn Arg Cys Phe Thr Ala Tyr Pro Thr Ser
65             70             75             80

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Met Pro Asp Tyr Phe Lys Gln Ala Phe Pro Asp Gly Met Ser Tyr Glu  
85 90 95  
Arg Thr Phe Thr Tyr Glu Asp Gly Gly Val Ala Thr Ala Ser Trp Glu  
100 105 110  
Ile Ser Leu Lys Gly Asn Cys Phe Glu His Lys Ser Thr Phe His Gly  
115 120 125  
Val Asn Phe Pro Ala Asp Gly Pro Val Met Ala Lys Met Thr Thr Gly  
130 135 140  
Trp Asp Pro Ser Phe Glu Lys Met Thr Val Cys Asp Gly Ile Leu Lys  
145 150 155 160  
Gly Asp Val Thr Ala Phe Leu Met Leu Gln Gly Gly Gly Asn Tyr Arg  
165 170 175  
Cys Gln Phe His Thr Ser Tyr Lys Thr Lys Lys Pro Val Thr Met Pro  
180 185 190  
Pro Asn His Ala Val Glu His Arg Ile Ala Arg Thr Asp Leu Asp Lys  
195 200 205  
Gly Gly Asn Ser Val Gln Leu Thr Glu His Ala Val Ala His Ile Thr  
210 215 220  
Ser Val Val Pro Phe  
225

<210> 3  
<211> 693  
<212> DNA  
<213> Zoanthus sp.

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tgcgtcgcgat gacataaatt tgtgatcacg ggagagggca ttggatatcc gttcaaaggg 120  
aaacaggcta ttaattctgtg tgtggtcgaa ggtggaccat tgccatttgc cgaagacata 180  
ttgtcagctg cctttatgta cggaaacagg gttttcactg aatatcctca agacatagct 240  
gactatttca agaactcgtg tctgtctggt tatacatggg acaggtcttt tctctttgag 300  
gatggagcag tttgcatatg taatgcagat ataacagtga gtgttgaaga aaactgcatg 360  
tatcatgagt ccaaatttta tggagtgaat tttcctgctg atggacctgt gatgaaaaag 420  
atgacagata actgggagcc atcctgcgag aagatcatac cagtacctaa gcaggggata 480  
ttgaaagggg atgtctccat gtacctcctt ctgaaggatg gtgggcgttt acggtgccaa 540  
ttcgacacag tttacaaagc aaagtctgtg ccaagaaaga tgccggactg gcacttcatac 600  
cagcataagc tcacccgtga agaccgcagc gatgctaaga atcagaaatg gcatctgaca 660  
gaacatgcta ttgcatccgg atctgcattg ccc 693

<210> 4  
<211> 231  
<212> PRT  
<213> Zoanthus sp.

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20 25 30  
Gly Ile Gly Tyr Pro Phe Lys Gly Lys Gln Ala Ile Asn Leu Cys Val  
35 40 45  
Val Glu Gly Gly Pro Leu Pro Phe Ala Glu Asp Ile Leu Ser Ala Ala  
50 55 60  
Phe Asn Tyr Gly Asn Arg Val Phe Thr Glu Tyr Pro Gln Asp Ile Ala  
65 70 75 80  
Asp Tyr Phe Lys Asn Ser Cys Pro Ala Gly Tyr Thr Trp Asp Arg Ser  
85 90 95  
Phe Leu Phe Glu Asp Gly Ala Val Cys Ile Cys Asn Ala Asp Ile Thr

			100					105					110				
Val	Ser	Val	Glu	Glu	Asn	Cys	Met	Tyr	His	Glu	Ser	Lys	Phe	Tyr	Gly		
		115					120					125					
Val	Asn	Phe	Pro	Ala	Asp	Gly	Pro	Val	Met	Lys	Lys	Met	Thr	Asp	Asn		
	130					135					140						
Trp	Glu	Pro	Ser	Cys	Glu	Lys	Ile	Ile	Pro	Val	Pro	Lys	Gln	Gly	Ile		
145					150					155					160		
Leu	Lys	Gly	Asp	Val	Ser	Met	Tyr	Leu	Leu	Leu	Lys	Asp	Gly	Gly	Arg		
			165					170						175			
Leu	Arg	Cys	Gln	Phe	Asp	Thr	Val	Tyr	Lys	Ala	Lys	Ser	Val	Pro	Arg		
		180						185					190				
Lys	Met	Pro	Asp	Trp	His	Phe	Ile	Gln	His	Lys	Leu	Thr	Arg	Glu	Asp		
	195						200					205					
Arg	Ser	Asp	Ala	Lys	Asn	Gln	Lys	Trp	His	Leu	Thr	Glu	His	Ala	Ile		
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Ala	Ser	Gly	Ser	Ala	Leu	Pro											
225					230												

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 <211> 865  
 <212> DNA  
 <213> Zoanthus sp.

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 gtgctgaac ggacataaat ttgtgatcac gggcgaaggc attggatata cgttcaaagg 180  
 gaaacagact attaacttgt gtgtgatcga agggggacca ttgccatttt ccgaagacat 240  
 attgtcagct ggctttaagt acggagacag gatttttact gaatatcctc aagacatagt 300  
 agactatttc aagaactcgt gtcctgctgg atatacatgg ggcaggtctt ttctctttga 360  
 ggatggagca gtctgcatat gcaatgtaga tataacagtg agtgtcaaag aaaactgcat 420  
 ttatcataag agcatattta atggaatgaa ttttctgtct gatggacctg tgatgaaaaa 480  
 gatgacaact aactgggaag catcctgcga gaagatcatg ccagtaccta agcaggggat 540  
 actgaaaggg gatgtctcca tgtacctcct tctgaaggat ggtgggctgt accggtgcca 600  
 gttcgacaca gtttaciaaag caaagtctgt gccaaagtaag atgccggagt ggcacttcat 660  
 ccagcataag ctctccctgt aagaccgcag cgatgctaag aatcagaagt ggcagctgac 720  
 agagcatgct attgcattcc cttctgcctt ggcctgataa gaatgtagtt ccaacatttt 780  
 aatgcatgtg cttgtcaatt attctgataa aaatgtagtt gagttgaaaa cagacaagta 840  
 caaataaagc acatgtaaatt cgtct 865

<210> 6  
 <211> 230  
 <212> PRT  
 <213> Zoanthus sp.

<400> 6  
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 His Met Glu Gly Cys Val Asn Gly His Lys Phe Val Ile Thr Gly Glu  
 20 25 30  
 Gly Ile Gly Tyr Pro Phe Lys Gly Lys Gln Thr Ile Asn Leu Cys Val  
 35 40 45  
 Ile Glu Gly Gly Pro Leu Pro Phe Ser Glu Asp Ile Leu Ser Ala Gly  
 50 55 60  
 Phe Lys Tyr Gly Asp Arg Ile Phe Thr Glu Tyr Pro Gln Asp Ile Val  
 65 70 75 80  
 Asp Tyr Phe Lys Asn Ser Cys Pro Ala Gly Tyr Thr Trp Gly Ser Phe  
 85 90 95  
 Leu Phe Glu Asp Gly Ala Val Cys Ile Cys Asn Val Asp Ile Thr Val

			100					105					110				
Ser	Val	Lys	Glu	Asn	Cys	Ile	Tyr	His	Lys	Ser	Ile	Phe	Asn	Gly	Met		
		115					120					125					
Asn	Phe	Pro	Ala	Asp	Gly	Pro	Val	Met	Lys	Lys	Met	Thr	Thr	Asn	Trp		
	130					135					140						
Glu	Ala	Ser	Cys	Glu	Lys	Ile	Met	Pro	Val	Pro	Lys	Gln	Gly	Ile	Leu		
145				150						155					160		
Lys	Gly	Asp	Val	Ser	Met	Tyr	Leu	Leu	Leu	Lys	Asp	Gly	Gly	Arg	Tyr		
			165				170							175			
Arg	Cys	Gln	Phe	Asp	Thr	Val	Tyr	Lys	Ala	Lys	Ser	Val	Pro	Ser	Lys		
		180					185						190				
Met	Pro	Glu	Trp	His	Phe	Ile	Gln	His	Lys	Leu	Leu	Arg	Glu	Asp	Arg		
	195						200					205					
Ser	Asp	Ala	Lys	Asn	Gln	Lys	Trp	Gln	Leu	Thr	Glu	His	Ala	Ile	Ala		
	210					215					220						
Phe	Pro	Ser	Ala	Leu	Ala												
225					230												

<210> 7  
 <211> 678  
 <212> DNA  
 <213> Discosoma sp

<400> 7  
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 cacaacaccg tgaagctgaa ggtgaccaag ggcggccccc tgcccttcgc ctgggacatc 180  
 ctgtcccccc agttccagta cggctccaag gtgtacgtga agcaccgccg cgacatcccc 240  
 gactacaaga agctgtcctt ccccgagggc ttcaagtggg agcgcgtgat gaacttcgag 300  
 gacggcgggc tggtgaccgt gaccacggac tcctccctgc aggacggctg cttcatctac 360  
 aaggtgaagt tcatcggcgt gaacttcccc tccgacggcc ccgtgatgca gaagaagacc 420  
 atgggctggg aggcctccac cgagcgccctg taccctccgc acggcgtgct gaagggcgag 480  
 atccacaagg ccctgaagct gaaggacggc ggccactacc tggtggagtt caagtccatc 540  
 tacatggcca agaagcccgt gcagctgccc ggctactact acgtggactc caagctggac 600  
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 caccacctgt tcctgtaa 678

<210> 8  
 <211> 225  
 <212> PRT  
 <213> Discosoma sp.

<400> 8  
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 Arg Met Glu Gly Thr Val Asn Gly His Glu Phe Glu Ile Glu Gly Glu  
 20 25 30  
 Gly Glu Gly Arg Pro Tyr Glu Gly His Asn Thr Val Lys Leu Lys Val  
 35 40 45  
 Thr Lys Gly Gly Pro Leu Pro Phe Ala Trp Asp Ile Leu Ser Pro Gln  
 50 55 60  
 Phe Gln Tyr Gly Ser Lys Val Tyr Val Lys His Pro Ala Asp Ile Pro  
 65 70 75 80  
 Asp Tyr Lys Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val  
 85 90 95  
 Met Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser  
 100 105 110  
 Leu Gln Asp Gly Cys Phe Ile Tyr Lys Val Lys Phe Ile Gly Val Asn  
 115 120 125

Phe Pro Ser Asp Gly Pro Val Met Gln Lys Lys Thr Met Gly Trp Glu  
 130 135 140  
 Ala Ser Thr Glu Arg Leu Tyr Pro Arg Asp Gly Val Leu Lys Gly Glu  
 145 150 155 160  
 Ile His Lys Ala Leu Lys Leu Lys Asp Gly Gly His Tyr Leu Val Glu  
 165 170 175  
 Phe Lys Ser Ile Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Tyr  
 180 185 190  
 Tyr Tyr Val Asp Ser Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr  
 195 200 205  
 Thr Ile Val Glu Gln Tyr Glu Arg Thr Glu Gly Arg His His Leu Phe  
 210 215 220  
 Leu  
 225

<210> 9  
 <211> 696  
 <212> DNA  
 <213> *Anemonia sulcata*

<400> 9  
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 atgaagatag aggtcatcga aggaggtcca ttgccatttg ccttcacat tttgtcaacg 180  
 agttgtatgt acggtagtaa ggccttcacg aagtatgtgt caggaattcc tgactacttc 240  
 aagcagtcct tccctgaagg ttttacttgg gaaagaacca caacctacga ggatggaggc 300  
 tttcttacag ctcatcagga cacaagccta gatggagatt gcctcgttta caaggtcaag 360  
 attcttggtg ataattttcc tgctgatggc cccgtgatgc agaacaaagc aggaagatgg 420  
 gagccatcca ccgagatagt ttatgaagtt gacgggtgtcc tgcgtggaca gtctttgatg 480  
 gcccttaagt gccctggtgg tcgtcatctg acttgccatc tccatactac ttacaggtcc 540  
 aaaaaaccag ctgctgcctt gaagatgccg ggatttcatt ttgaagatca tcgcatcgag 600  
 ataatggagg aagttgagaa aggcaagtgc tataaacagt acgaagcagc agtgggcagg 660  
 tactgtgatg ctgctccatc caagcttggg cataac 696

<210> 10  
 <211> 232  
 <212> PRT  
 <213> *Anemonia sulcata*

<400> 10  
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 Gly Thr Val Asn Gly His Tyr Phe Lys Cys Thr Gly Lys Gly Glu Gly  
 20 25 30  
 Asn Pro Phe Glu Gly Thr Gln Glu Met Lys Ile Glu Val Ile Glu Gly  
 35 40 45  
 Gly Pro Leu Pro Phe Ala Phe His Ile Leu Ser Thr Ser Cys Met Tyr  
 50 55 60  
 Gly Ser Lys Thr Phe Ile Lys Tyr Val Ser Gly Ile Pro Asp Tyr Phe  
 65 70 75 80  
 Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr  
 85 90 95  
 Glu Asp Gly Gly Phe Leu Thr Ala His Gln Asp Thr Ser Leu Asp Gly  
 100 105 110  
 Asp Cys Leu Val Tyr Lys Val Lys Ile Leu Gly Asn Asn Phe Pro Ala  
 115 120 125  
 Asp Gly Pro Val Met Gln Asn Lys Ala Gly Arg Trp Glu Pro Ala Thr  
 130 135 140  
 Glu Ile Val Tyr Glu Val Asp Gly Val Leu Arg Gly Gln Ser Leu Met

145		150		155		160									
Ala	Leu	Lys	Cys	Pro	Gly	Gly	Arg	His	Leu	Thr	Cys	His	Leu	His	Thr
		165		170		175									
Thr	Tyr	Arg	Ser	Lys	Lys	Pro	Ala	Ala	Ala	Leu	Lys	Met	Pro	Gly	Phe
		180		185		190									
His	Phe	Glu	Asp	His	Arg	Ile	Glu	Ile	Met	Glu	Glu	Val	Glu	Lys	Gly
		195		200		205									
Lys	Cys	Tyr	Lys	Gln	Tyr	Glu	Ala	Ala	Val	Gly	Arg	Tyr	Cys	Asp	Ala
		210		215		220									
Ala	Pro	Ser	Lys	Leu	Gly	His	Asn								
225				230											

<210> 11  
 <211> 678  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> hybrid coding sequence

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 cactgcagcg tgaagctcat ggtgaccaag ggcggccccc tccccttcgc cttcgacatc 180  
 ctcagccccc agttccagta cggcagcaag gtgtacgtga agcaccgccg cgacatcccc 240  
 gactacaaga agctcagctt ccccgagggc ttcaagtggg agcgggtgat gaacttcgag 300  
 gacggcggcg tggtagccgt gagccaggac agcagcctca aggacggctg cttcatctac 360  
 gaggtgaagt tcatcgccgt gaacttcccc agcgacggcc ccgtgatgca gcggcggacc 420  
 cggggctggg aggccagcag cgagcggctc taccgccggg acggcgtgct caagggcgac 480  
 atccacatgg cctccggct cgagggcggc ggccactacc tcgtggagtt caagagcatc 540  
 tacatggcca agaagcccgt gcagctcccc ggctactact acgtggacag caagctcgac 600  
 atcaccagcc acaacgagga ctacaccatc gtggagcagt acgagcggac cgagggccgg 660  
 caccacctct tcctctga 678

<210> 12  
 <211> 225  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> hybrid protein

<400> 12  
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 20 25 30  
 Gly Glu Gly Arg Pro Tyr Glu Gly His Cys Ser Val Lys Leu Met Val  
 35 40 45  
 Thr Lys Gly Gly Pro Leu Pro Phe Ala Phe Asp Ile Leu Ser Pro Gln  
 50 55 60  
 Phe Gln Tyr Gly Ser Lys Val Tyr Val Lys His Pro Ala Asp Ile Pro  
 65 70 75 80  
 Asp Tyr Lys Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val  
 85 90 95  
 Met Asn Phe Glu Asp Gly Gly Val Val Thr Val Ser Gln Asp Ser Ser  
 100 105 110  
 Leu Lys Asp Gly Cys Phe Ile Tyr Glu Val Lys Phe Ile Gly Val Asn  
 115 120 125

Phe Pro Ser Asp Gly Pro Val Met Gln Arg Arg Thr Arg Gly Trp Glu  
 130 135 140  
 Ala Ser Ser Glu Arg Leu Tyr Pro Arg Asp Gly Val Leu Lys Gly Asp  
 145 150 155 160  
 Ile His Met Ala Leu Arg Leu Glu Gly Gly Gly His Tyr Leu Val Glu  
 165 170 175  
 Phe Lys Ser Ile Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Tyr  
 180 185 190  
 Tyr Tyr Val Asp Ser Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr  
 195 200 205  
 Thr Ile Val Glu Gln Tyr Glu Arg Thr Glu Gly Arg His His Leu Phe  
 210 215 220  
 Leu  
 225

<210> 13  
 <211> 675  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> non-aggregating mutant

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 accgtgaacg gccacgagtt cgagatcgag ggcgagggcg agggccgccc ctacgagggc 120  
 cacaacaccg tgaagctgaa ggtgaccaag ggcggccccc tgcccttcgc ctgggacatc 180  
 ctgtcccccc agttccagta cggctccaag gtgtacgtga agcaccgccg cgacatcccc 240  
 gactacaaga agctgtcctt ccccgagggc ttcaagtggg agcgcgatgat gaacttcgag 300  
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 aaggtgaagt tcatcggcgt gaacttcccc tccgacggcc ccgtgatgca gaagaagacc 420  
 atgggctggg aggcctccac cgagcgctg taccgccgag acggcggtgct gaagggcgag 480  
 acccacaagg ccctgaagct gaaggacggc ggccactacc tgggtggagtt caagtccatc 540  
 tacatggcca agaagcccgt gcagctgccc ggctactact acgtggacgc caagctggac 600  
 atcacctccc acaacgagga ctacaccatc gtggagcagt acgagcgcac cgagggccgc 660  
 caccacctgt tcctg 675

<210> 14  
 <211> 678  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> non-aggregating mutant

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 cacaacaccg tgaagttgaa ggtgaccaag ggcggccccc tgcccttcgc ctgggacatc 180  
 ctgtcccccc agttccagta cggctccaag gtgtacgtga agcaccgccg cgacatcccc 240  
 gactacaaga agctgtcctt ccccgagggc ttcaagtggg agcgcgatgat gaacttcgag 300  
 gacggcgggc tggcgaccgt gaccagggac tcctccctgc aggacggctg cttcatctac 360  
 aaggtgaagt tcatcggcgt gaacttcccc tccgacggcc ccgtgatgca gaagaagacc 420  
 atgggctggg aggcctccac cgagcgctg taccgccgag acggcggtgct gaagggcgag 480  
 atccacaagg ccctgaagct gaaggacggc ggccactacc tgggtggagtt caagtccatc 540  
 tacatggcca agaagcccgt gcagctgccc ggctactact acgtggacac caagctggac 600  
 atcacctccc acaacgagga ctacaccatc gtggagcagt acgagcgcac cgagggccgc 660  
 caccacctgt tcctgtaa 678

<210> 15  
 <211> 705  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> non-aggregating mutant

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 gggaaacagg ctattaatct gtgtgtgggtc gaagggtggac cattgccatt tgcogaagac 180  
 atattgtcag ctgcctttat gtacggaaac agggttttca ctgaatatcc tcaagacata 240  
 gttgactatt tcaagaactc gtgtcctgct ggatatacat gggacaggtc ttttctcttt 300  
 gaggatggag cagtttgcac atgtaatgca gatataacag tgagtgttga agaaaactgc 360  
 atgtatcatg agtccaaatt ctatggagtg aattttcctg ctgatggacc tgtgatgaaa 420  
 aagatgacag ataactggga gccatcctgc gagaagatca taccagtacc taagcagggg 480  
 atattgaaag gggatgtctc catgtacctc cttctgaagg atgggtgggcg tttacgggtgc 540  
 caattcgaca cagttttaca agcaaagtct gtgccaagaa agatgccgga ctggcacttc 600  
 atccagcata agctcaccgc tgaagaccgc agcgatgcta agaatacagaa atggcatctg 660  
 acagaacatg ctattgcatc cggatctgca ttgccctgaa agctt 705

<210> 16  
 <211> 230  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> non-aggregating mutant

<400> 16  
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 20 25 30  
 Ile Gly Tyr Pro Phe Lys Gly Lys Gln Thr Ile Asn Leu Cys Val Ile  
 35 40 45  
 Glu Gly Gly Pro Leu Pro Phe Ser Glu Asp Ile Leu Ser Ala Gly Phe  
 50 55 60  
 Lys Tyr Gly Asp Arg Ile Phe Thr Glu Tyr Pro Gln Asp Ile Val Asp  
 65 70 75 80  
 Tyr Phe Lys Asn Ser Cys Pro Ala Gly Tyr Thr Trp Gly Arg Ser Phe  
 85 90 95  
 Leu Phe Glu Asp Gly Ala Val Cys Ile Cys Asn Val Asp Ile Thr Val  
 100 105 110  
 Ser Val Lys Glu Asn Cys Ile Tyr His Lys Ser Ile Phe Asn Gly Val  
 115 120 125  
 Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Met Thr Thr Asn Trp  
 130 135 140  
 Glu Ala Ser Cys Glu Lys Ile Met Pro Val Pro Lys Gln Gly Ile Leu  
 145 150 155 160  
 Lys Gly Asp Val Ser Met Tyr Leu Leu Leu Lys Asp Gly Gly Arg Tyr  
 165 170 175  
 Arg Cys Gln Phe Asp Thr Val Tyr Lys Ala Lys Ser Val Pro Ser Lys  
 180 185 190  
 Met Pro Glu Trp His Phe Ile Gln His Lys Leu Leu Arg Glu Asp Arg  
 195 200 205  
 Ser Asp Ala Lys Asn Gln Lys Trp Gln Leu Thr Glu His Ala Ile Ala  
 210 215 220  
 Phe Pro Ser Ala Leu Ala



<210> 17  
 <211> 705  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> non-aggregating mutant

<400> 17  
 ggatccgccc acagcgagca cggcctgacc gaggagatga ccatgaagta ccacatggag 60  
 ggctgcgtga acggccacaa gttcgtgata accggcgagg gcatcggtta ccccttcaag 120  
 ggcaagcaga ccatcaacct gtgcgtgata gagggcggcc ccctgccctt cagcgaggac 180  
 atcctgagcg ccggcttcaa gtacggcgac cggatcttca ccgagtaccc ccaggacatc 240  
 gtggactact tcaagaacag ctgccccgcc ggctacacct ggggccggag cttcctgttc 300  
 gaggacggcg ccgtgtgcat ctgtaacgtg gacatcaccg tgagcgtgaa ggagaactgc 360  
 atctaccaca agagcatctt caacggcgtg aacttccccg ccgacggccc cgtgatgaag 420  
 aagatgacca ccaactggga ggccagctgc gagaagatca tgcccgtgcc taagcagggc 480  
 atcctgaagg ggcacgtgag catgtacctg ctgctgaagg acggcggccg gtaccgggtc 540  
 cagttcgaca ccgtgtacaa ggccaagagc gtgcccagca agatgcccga gtggcacttc 600  
 atccagcaca agctgctgcg ggaggaccgg agcgacgcca agaaccagaa gtggcagctg 660  
 accgagcacg ccatcgccctt ccccgcgccc ctggcctgaa agctt 705

<210> 18  
 <211> 230  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> non-aggregating mutant

<400> 18  
 Ala His Ser Glu His Gly Leu Thr Glu Glu Met Thr Met Lys Tyr His  
 1 5 10 15  
 Met Glu Gly Cys Val Asn Gly His Lys Phe Val Ile Thr Gly Glu Gly  
 20 25 30  
 Ile Gly Tyr Pro Phe Lys Gly Lys Gln Thr Ile Asn Leu Cys Val Ile  
 35 40 45  
 Glu Gly Gly Pro Leu Pro Phe Ser Glu Asp Ile Leu Ser Ala Gly Phe  
 50 55 60  
 Lys Tyr Gly Asp Arg Ile Phe Thr Glu Tyr Pro Gln Asp Ile Val Asp  
 65 70 75 80  
 Tyr Phe Lys Asn Ser Cys Pro Ala Gly Tyr Thr Trp Gly Arg Ser Phe  
 85 90 95  
 Leu Phe Glu Asp Gly Ala Val Cys Ile Cys Asn Val Asp Ile Thr Val  
 100 105 110  
 Ser Val Lys Glu Asn Cys Ile Tyr His Lys Ser Ile Phe Asn Gly Val  
 115 120 125  
 Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Met Thr Thr Asn Trp  
 130 135 140  
 Glu Ala Ser Cys Glu Lys Ile Met Pro Val Pro Lys Gln Gly Ile Leu  
 145 150 155 160  
 Lys Gly Asp Val Ser Met Tyr Leu Leu Leu Lys Asp Gly Gly Arg Tyr  
 165 170 175  
 Arg Cys Gln Phe Asp Thr Val Tyr Lys Ala Lys Ser Val Pro Ser Lys  
 180 185 190  
 Met Pro Glu Trp His Phe Ile Gln His Lys Leu Leu Arg Glu Asp Arg  
 195 200 205

Ser Asp Ala Lys Asn Gln Lys Trp Gln Leu Thr Glu His Ala Ile Ala  
 210 215 220  
 Phe Pro Ser Ala Leu Ala  
 225 230

<210> 19  
 <211> 690  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> non-aggregating mutant

<400> 19  
 atggccctgt ccaacgagtt catcggcgac gacatgaaga tgacctacca catggacggc 60  
 tgcgtgaacg gccactactt caccgtgaag ggcgagggca gcggcaagcc ctacgagggc 120  
 acccagacct ccaccttcaa ggtgaccatg gccaacggcg gcccctggc cttctccttc 180  
 gacatcctgt ccacgtgtt catgtacggc aaccgtgtct tcaccgccta cccaccagc 240  
 atgcccgaact acttcaagca ggccttcccc gacggcatgt cctacgagag aaccttcacc 300  
 tacgaggacg gcggcggtggc caccgccagc tgggagatca gcctgaaggc caactgcttc 360  
 gagcacaagt ccaccttcca cggcggtgaac ttccccgccg acggccccgt gatggccaag 420  
 aagaccaccg gctgggaccc ctccctcgag aagatgaccg tgtgcgacgg catcttgaag 480  
 ggcgacgtga ccgccttcct gatgctgcag ggcgggcgga actacagatg ccagttccac 540  
 acctcctaca agaccaagaa gcccgtgacc atgcccccca accacgtggt ggagcaccgc 600  
 atcgccagaa ccgacctgga caagggcggc aacagcgtgc agctgaccga gcacgccgtg 660  
 gccacatca cctccgtggt gcccttctga 690

<210> 20  
 <211> 229  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> non-aggregating mutant

<400> 20  
 Met Ala Leu Ser Asn Glu Phe Ile Gly Asp Asp Met Lys Met Thr Tyr  
 1 5 10 15  
 His Met Asp Gly Cys Val Asn Gly His Tyr Phe Thr Val Lys Gly Glu  
 20 25 30  
 Gly Ser Gly Lys Pro Tyr Glu Gly Thr Gln Thr Ser Thr Phe Lys Val  
 35 40 45  
 Thr Met Ala Asn Gly Gly Pro Leu Ala Phe Ser Phe Asp Ile Leu Ser  
 50 55 60  
 Thr Val Phe Met Tyr Gly Asn Arg Cys Phe Thr Ala Tyr Pro Thr Ser  
 65 70 75 80  
 Met Pro Asp Tyr Phe Lys Gln Ala Phe Pro Asp Gly Met Ser Tyr Glu  
 85 90 95  
 Arg Thr Phe Thr Tyr Glu Asp Gly Gly Val Ala Thr Ala Ser Trp Glu  
 100 105 110  
 Ile Ser Leu Lys Gly Asn Cys Phe Glu His Lys Ser Thr Phe His Gly  
 115 120 125  
 Val Asn Phe Pro Ala Asp Gly Pro Val Met Ala Lys Lys Thr Thr Gly  
 130 135 140  
 Trp Asp Pro Ser Phe Glu Lys Met Thr Val Cys Asp Gly Ile Leu Lys  
 145 150 155 160  
 Gly Asp Val Thr Ala Phe Leu Met Leu Gln Gly Gly Gly Asn Tyr Arg  
 165 170 175  
 Cys Gln Phe His Thr Ser Tyr Lys Thr Lys Lys Pro Val Thr Met Pro



Leu	Glu	Cys	Pro	Gly	Gly	Arg	His	Leu	Thr	Cys	His	Leu	His	Thr	Thr
				165					170					175	
Tyr	Arg	Ser	Lys	Lys	Pro	Ala	Ser	Ala	Leu	Lys	Met	Pro	Gly	Phe	His
			180					185					190		
Phe	Glu	Asp	His	Arg	Ile	Glu	Ile	Leu	Glu	Glu	Val	Glu	Lys	Gly	Lys
		195				200						205			
Cys	Tyr	Lys	Gln	Tyr	Glu	Ala	Ala	Val	Gly	Arg	Tyr	Cys	Asp	Ala	Ala
	210					215					220				
Pro	Ser	Lys	Leu	Gly	His	Asn									
225					230										

<210> 23

<211> 654

<212> DNA

<213> Artificial Sequence

<220>

<223> non-aggregating mutant

<400> 23

gagggcaccg	tgaacggcca	ctacttcaag	tgcaccggca	agggcgaggg	caaccccctc	60
gagggcaccc	aggagatgaa	gatcgaggtg	atcgagggcg	gccccctgcc	cttcgccttc	120
cacatcctgt	ccacctcctg	catgtacggc	tccaaggcct	tcatcaagta	cgtgtccggc	180
atccccgact	acttcaagca	gtccctcccc	gagggcttca	cctgggagcg	caccaccacc	240
tacgaggacg	gcggttcct	gaccgcccac	caggacacct	ccctggacgg	cgactgctg	300
gtgtacaagg	tgaagatcct	gggcaacaac	ttccccgccg	acggccccgt	gatgcagaac	360
aaggccggcc	gctgggagcc	ctccaccgag	atcgtgtacg	aggtggacgg	cgtgctgcgc	420
ggccagtcca	gcatggccct	ggagtgcccc	ggcggtcgcc	acctgacctg	ccacctgcac	480
accacctacc	gctccaagaa	gcccgcctcc	gccctgaaga	tgcccggctt	ccacttcgag	540
gaccaccgca	tcgagatcct	ggaggaggtg	gagaagggca	agtgctacaa	gcagtacgag	600
gccgccgtgg	gccgctactg	cgacgcgcgc	ccctccaagc	tgggccacaa	ctga	654

<210> 24

<211> 232

<212> PRT

<213> Artificial Sequence

<220>

<223> non-aggregating mutant

<400> 24

Met	Ala	Ser	Leu	Leu	Thr	Glu	Thr	Met	Pro	Phe	Arg	Thr	Thr	Ile	Glu
1			5					10						15	
Gly	Thr	Val	Asn	Gly	His	Tyr	Phe	Lys	Cys	Thr	Gly	Lys	Gly	Glu	Gly
			20					25					30		
Asn	Pro	Leu	Glu	Gly	Thr	Gln	Glu	Met	Lys	Ile	Glu	Val	Ile	Glu	Gly
		35				40					45				
Gly	Pro	Leu	Pro	Phe	Ala	Phe	His	Ile	Leu	Ser	Thr	Ser	Cys	Met	Tyr
	50				55						60				
Gly	Ser	Lys	Ala	Phe	Ile	Lys	Tyr	Val	Ser	Gly	Ile	Pro	Asp	Tyr	Phe
65					70					75				80	
Lys	Gln	Ser	Leu	Pro	Glu	Gly	Phe	Thr	Trp	Glu	Arg	Thr	Thr	Thr	Tyr
			85					90						95	
Glu	Asp	Gly	Gly	Phe	Leu	Thr	Ala	His	Gln	Asp	Thr	Ser	Leu	Asp	Gly
		100					105					110			
Asp	Cys	Leu	Val	Tyr	Lys	Val	Lys	Ile	Leu	Gly	Asn	Asn	Phe	Pro	Ala
	115						120					125			
Asp	Gly	Pro	Val	Met	Gln	Asn	Lys	Ala	Gly	Arg	Trp	Glu	Pro	Ser	Thr
	130					135					140				

Glu	Ile	Val	Tyr	Glu	Val	Asp	Gly	Val	Leu	Arg	Gly	Gln	Ser	Ser	Met
145					150					155					160
Ala	Leu	Glu	Cys	Pro	Gly	Gly	Arg	His	Leu	Thr	Cys	His	Leu	His	Thr
				165					170						175
Thr	Tyr	Arg	Ser	Lys	Lys	Pro	Ala	Ser	Ala	Leu	Lys	Met	Pro	Gly	Phe
			180					185					190		
His	Phe	Glu	Asp	His	Arg	Ile	Glu	Ile	Leu	Glu	Glu	Val	Glu	Lys	Gly
		195					200					205			
Lys	Cys	Tyr	Lys	Gln	Tyr	Glu	Ala	Ala	Val	Gly	Arg	Tyr	Cys	Asp	Ala
	210					215				220					
Ala	Pro	Ser	Lys	Leu	Gly	His	Asn								
225					230										

<210> 25  
 <211> 26  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> non-aggregating mutant fragment

Met	Arg	Ser	Ser	Lys	Asn	Val	Ile	Lys	Glu	Phe	Met	Arg	Phe	Lys	Val
1				5					10					15	
Arg	Met	Glu	Gly	Thr	Val	Asn	Gly	His	Glu						
			20					25							

<210> 26  
 <211> 26  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> non-aggregating mutant fragment

Met	Ser	Cys	Ser	Lys	Asn	Val	Ile	Lys	Glu	Phe	Met	Arg	Phe	Gln	Val
1				5					10					15	
Arg	Met	Glu	Gly	Thr	Val	Asn	Gly	His	Glu						
			20					25							

<210> 27  
 <211> 26  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> non-aggregating mutant fragment

Met	Ala	Gln	Ser	Lys	His	Gly	Leu	Thr	Lys	Glu	Met	Thr	Met	Lys	Tyr
1				5					10					15	
Arg	Met	Glu	Gly	Cys	Val	Asp	Gly	His	Lys						
			20					25							

<210> 28

<211> 26  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> non-aggregating mutant fragment

<400> 28  
 Met Ala His Ser Lys His Gly Leu Lys Glu Glu Met Thr Met Lys Tyr  
 1 5 10 15  
 His Met Glu Gly Cys Val Asn Gly His Lys  
 20 25

<210> 29  
 <211> 26  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> non-aggregating mutant fragment

<400> 29  
 Met Ala Leu Ser Asn Lys Phe Ile Gly Asp Asp Met Lys Met Thr Tyr  
 1 5 10 15  
 His Met Asp Gly Cys Val Asn Gly His Tyr  
 20 25

<210> 30  
 <211> 23  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> non-aggregating mutant fragment

<400> 30  
 Met Ala Ser Phe Leu Lys Lys Thr Met Pro Phe Lys Thr Thr Ile Glu  
 1 5 10 15  
 Gly Thr Val Asn Gly His Tyr  
 20

<210> 31  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> purification tag

<400> 31  
 Met Arg His His His His His His Gly Ser  
 1 5 10